NOAA FISHERIES

Southwest Fisheries Science Center

8.1 Genetic tagging for monitoring and evaluation of salmonid hatcheries

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West Coast Science Centers
Protected Species Program Review

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Hatcheries in salmonid management

- Hatcheries are powerful tools for modifying salmonid populations. Modifications can be of negative, positive or neutral with respect to population/ESU viability and evolution.

- Considerations very different for large- and small-scale hatchery programs, and for different species.

- The Devil is in the Details! We must use science-based approach, informed by monitoring, to direct operations, evaluate where in the spectrum effects are occurring and mitigate appropriately

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- Tagging data are cory of monitoring and evaluation.
  Coded wire tags are the most commonly issued tag- over 1B in salmonids- but recovery rates are ~0.2%.

Parentage-based Tagging

- Highly efficient, intergenerational (pedigree-based) genetic tagging method
    - Genotype parents with polymorphic molecular markers (e.g. SNPs)
    - Sampling and genotyping in offspring generation with same markers
    - Large-scale parentage analysis to identify parents

- Information obtained for each tag recovery is nearly the same as for CWTs
- By genotyping two parents, you tag “all” of their of offspring and it requires no juvenile handling, but MUCH higher tagging rates feasible.
- Transform the way that we use population genetic data from allele frequency-based framework to an individual DNA fingerprint framework with all individual genotypes considered first as potential direct matches (recaptures) or as nodes in pedigrees involving other genotypes in the database(s).

Parentage-based tagging –the other stuff

In addition to stock-of-origin and cohort, PBT gives you large pedigrees

- Near parametric estimates of variance in family size
- Conduct large quantitative genetic studies of phenotype: run timing, age at maturity, disease resistance
- Map genes for phenotypic traits to locations in the genome
- Evaluate different hatchery/release practices and consequences for fecundity, marine survival and straying
- Estimate straying and reproductive success of strays
- Study relative productivity of hatchery and natural fish by sampling at weirs, fish ladders and carcasses (carefully)
- Same data can be used for GSI-stock of origin for ALL sampled fish.

Validation of parentage-based tagging

- Anderson and Garza (2006; Genetics) found that a 100 (SNP) marker genotype can identify parental pairs with false positive rate < 1 fish per 300,000 offspring. Feasible with current methodology (i.e. 96.96 arrays).

- Anderson (2012) described software for the large scale parent pair/offspring analysis with SNP markers.

- Economic and operational feasibility study led by SWFSC staff recently completed (Satterthwaite et al. 2015)

- Beginning to be widely implemented, primarily in Idaho and California

Parentage-based tagging in California hatcheries

Hatchery programs with current broodstock sampling

Steelhead: Russian River; Central Valley (four programs)

Coho salmon: Klamath River-Iron Gate; Russian River

Chinook salmon: Trinity River- spring and fall run; Feather & San Joaquin River- spring run; Sacramento- winter run

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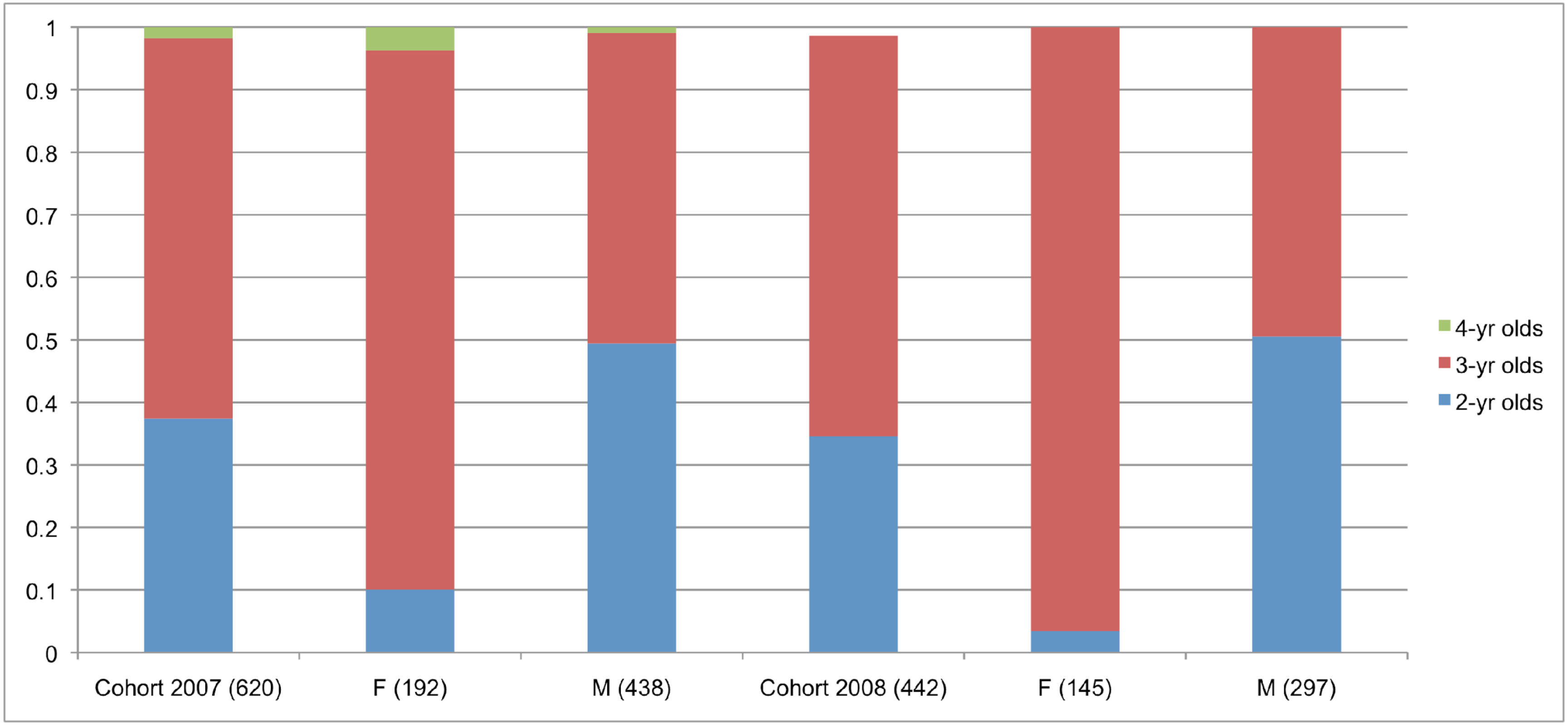
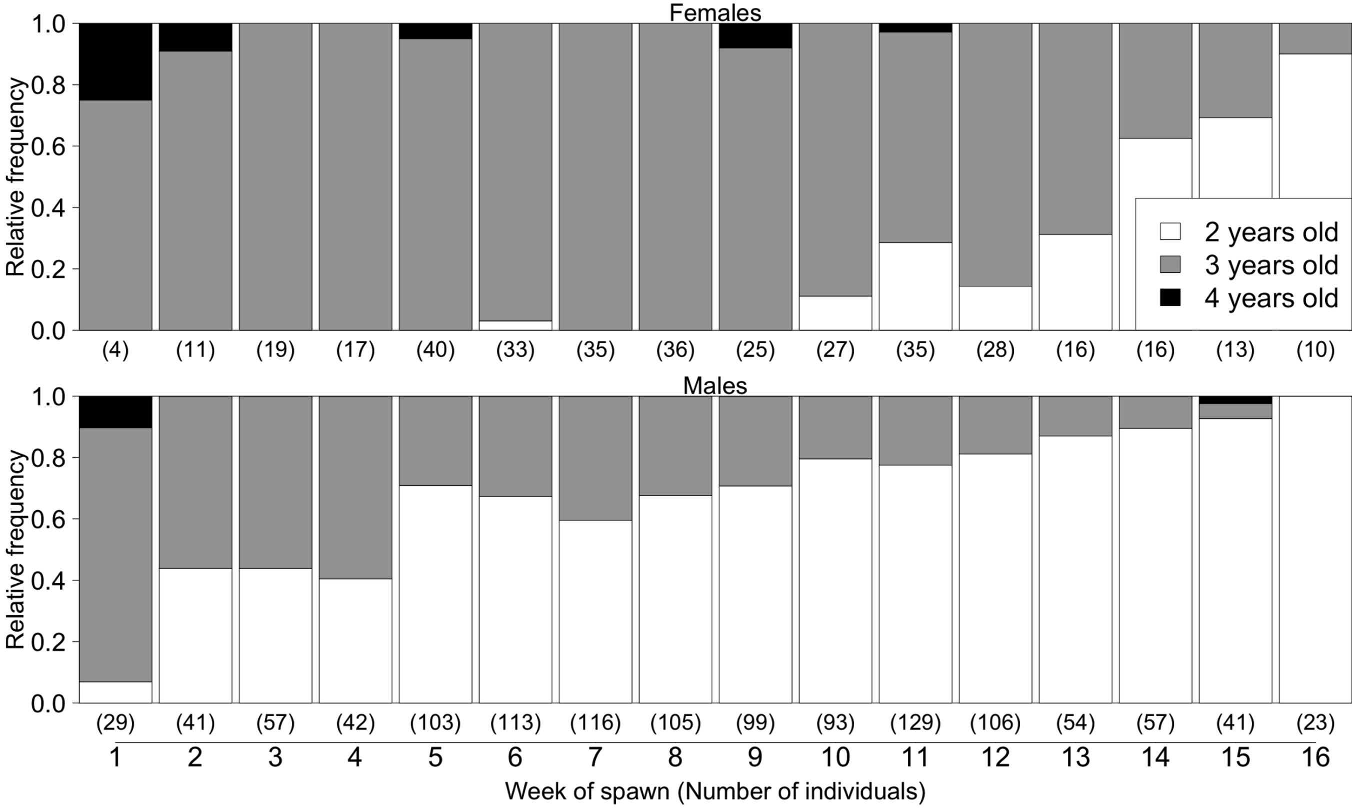
Steelhead and coho salmon mostly untagged.

Age structure of spawners: Russian River steelhead



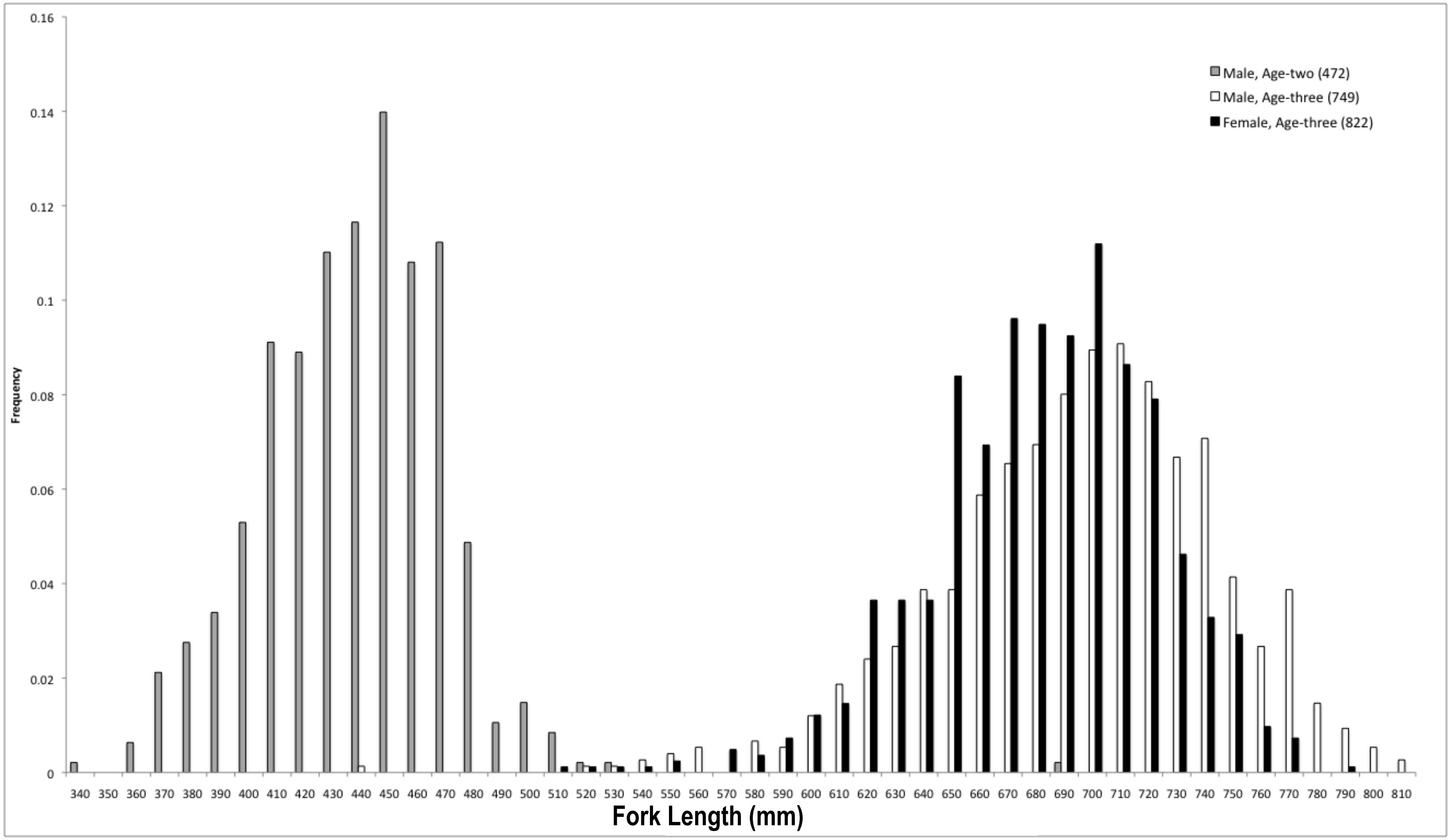
Abadía-Cardoso, Anderson, Pearse, Garza 2013 Molecular Ecology

Age structure of spawners: Russian River steelhead

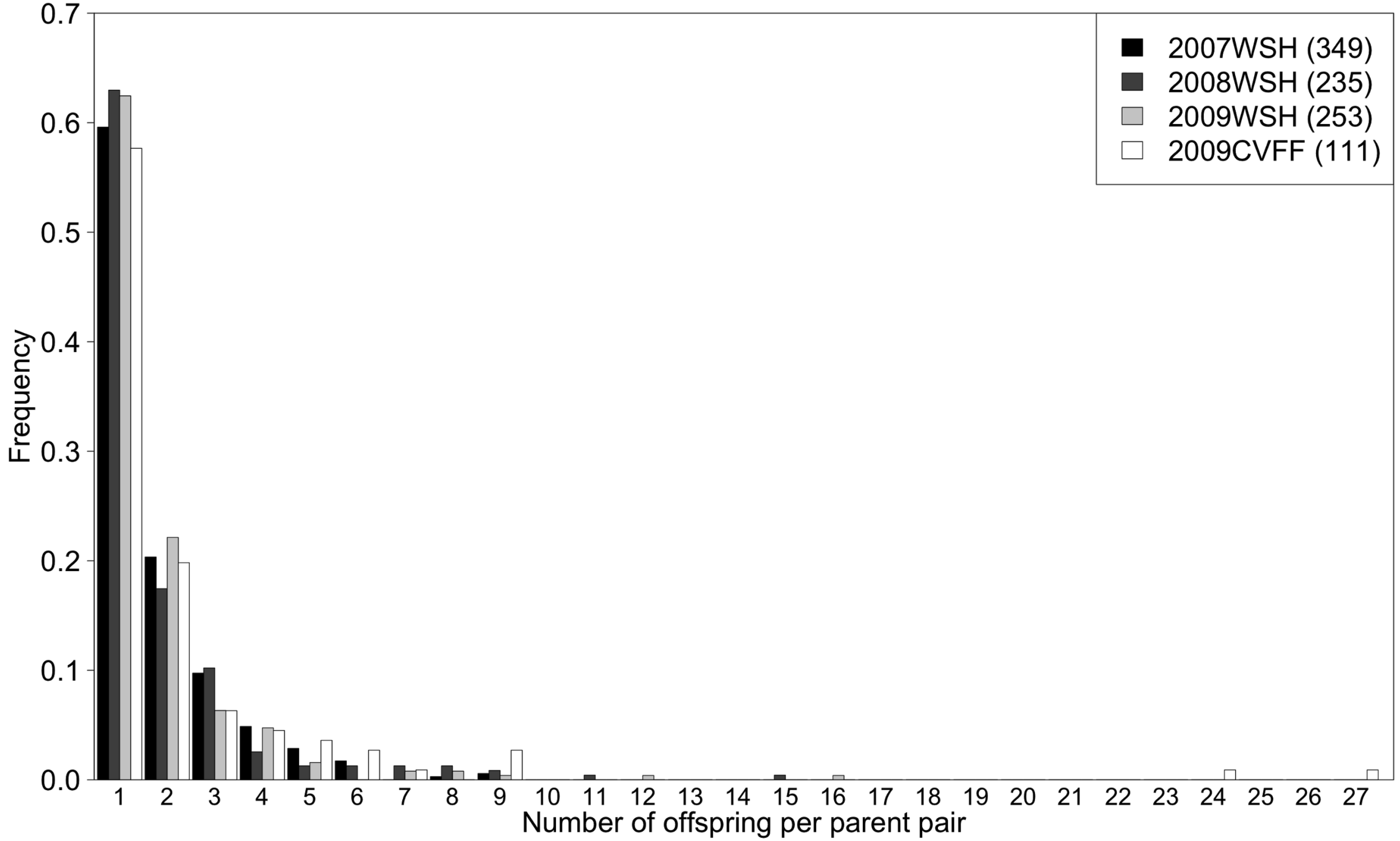


Two year olds return later than three year olds

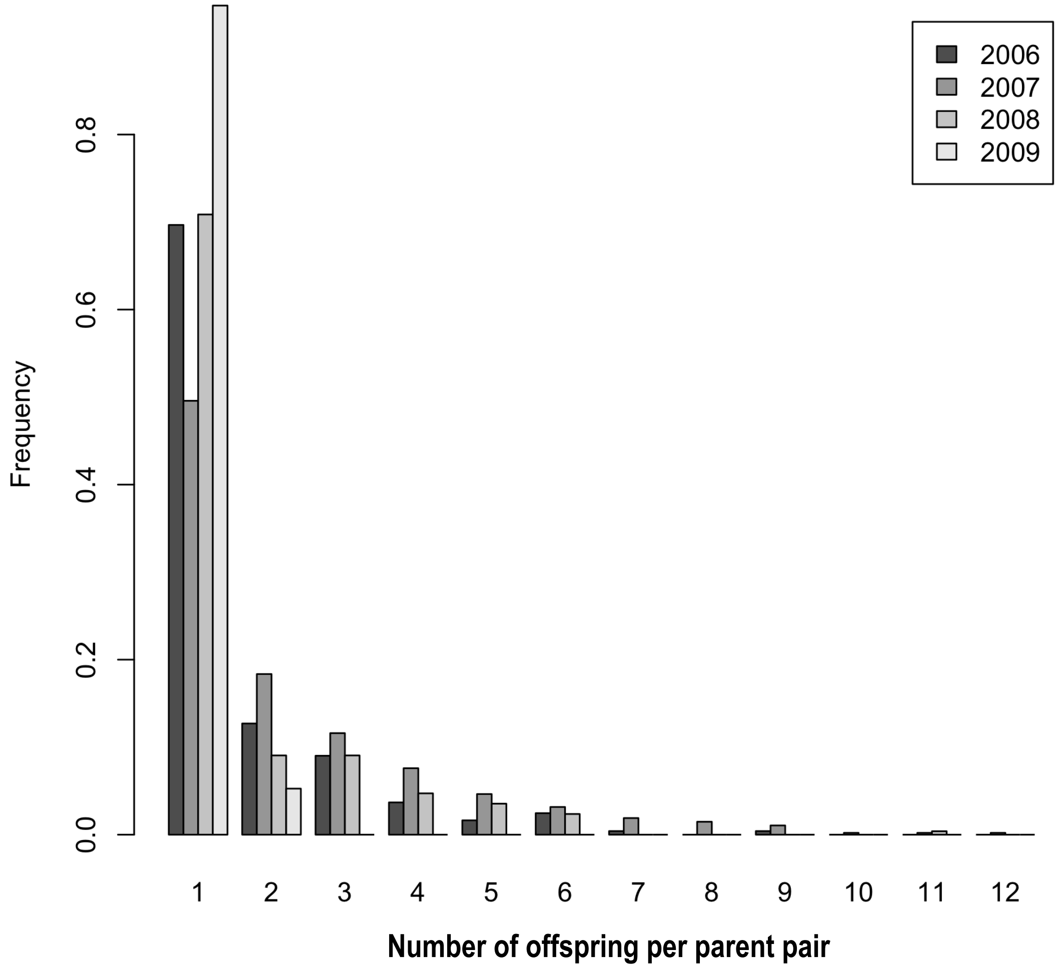
Age structure, size at age:
Klamath River coho salmon



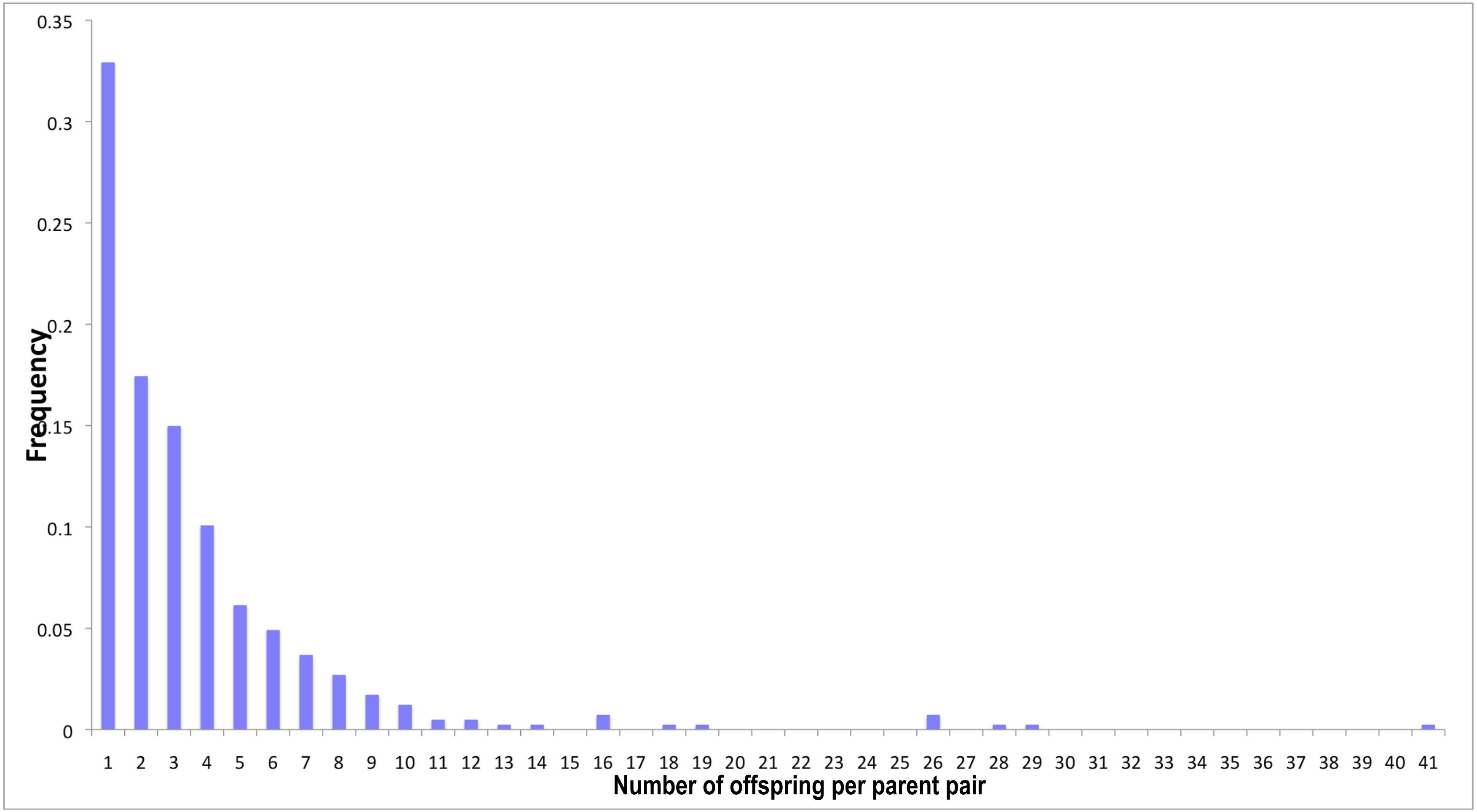
No. of offspring per parent pair: Russian River steelhead



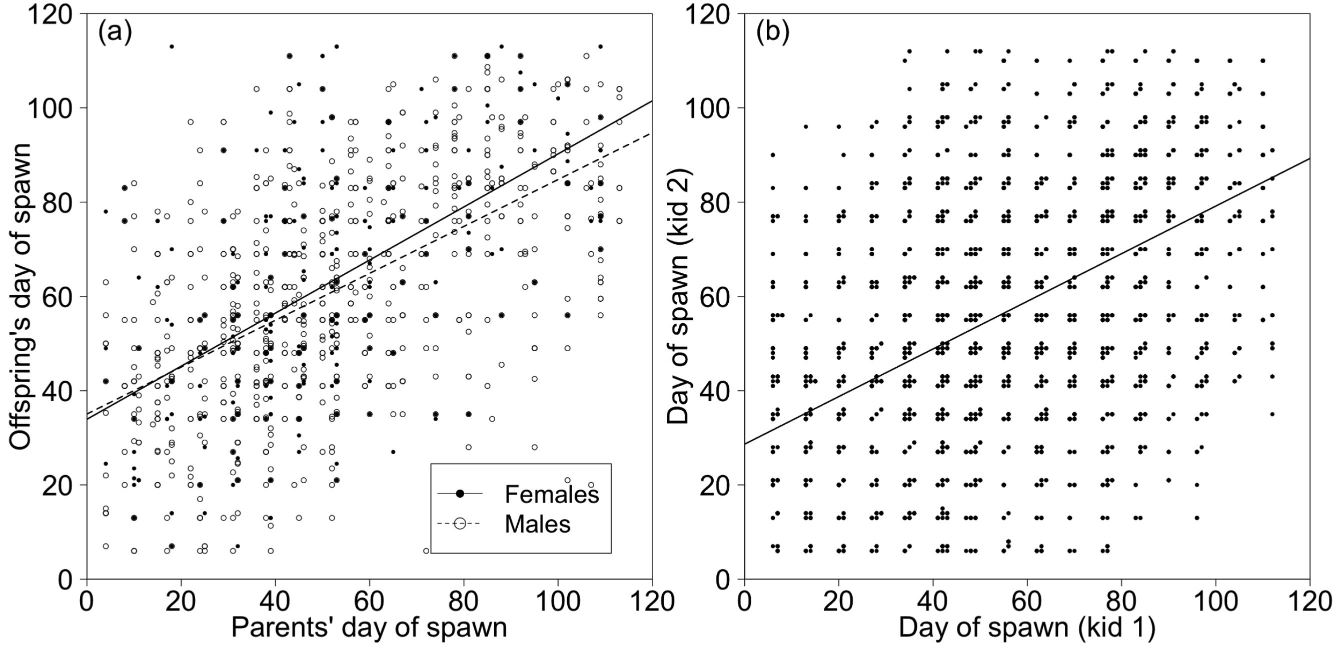
No. of offspring per parent pair: Feather River Chinook salmon



No. of offspring per parent pair: Klamath River coho salmon



Heritability of Run Timing: Russian River steelhead



Statistics-Males	
R^2	0.321
Heritability H^2	0.497

Statistics-Females	
R^2	0.320
Heritability H^2	0.563

Abadía-Cardoso, Anderson, Pearse, Garza 2013 Molecular Ecology

Iteroparity
Central Valley steelhead

Iteroparity
Matching samples analysis

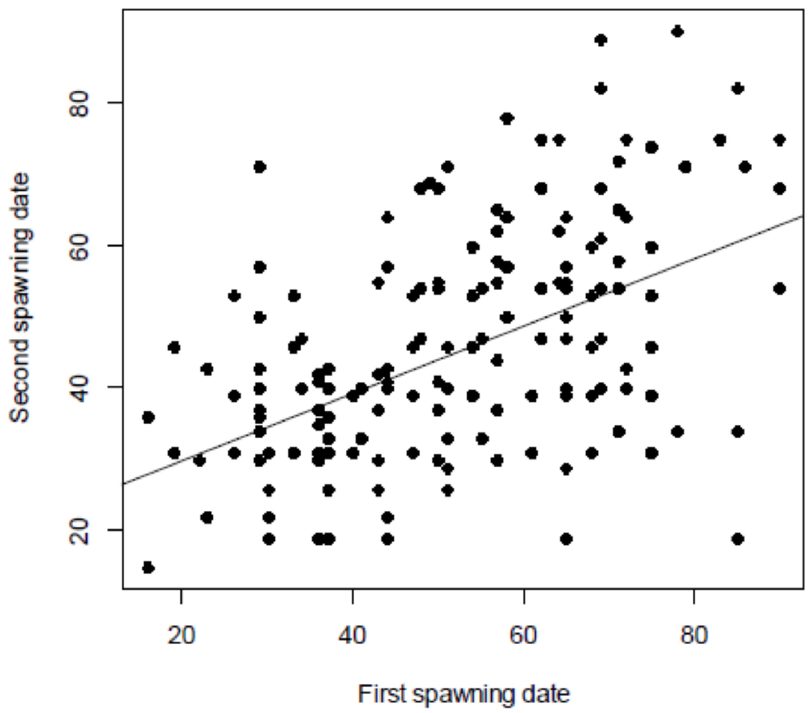
Hatchery program	Spawn year 2012	2013	2014
Coleman	33 (3.88%)	18 (2.01%)	36 (4.1%)
Feather River	26 (3.98%)	30 (2.56%)	73 (5.53%)
Nimbus	1 (0.39%)	0 (0%)	0 (0%)
Mokelumne River	11 (5.39%)	0 (0%)	3 (1.96%)

Iteroparous fish strongly biased towards females.

Iteroparity
Central Valley steelhead

Iteroparity and repeat spawning
Matching samples analysis

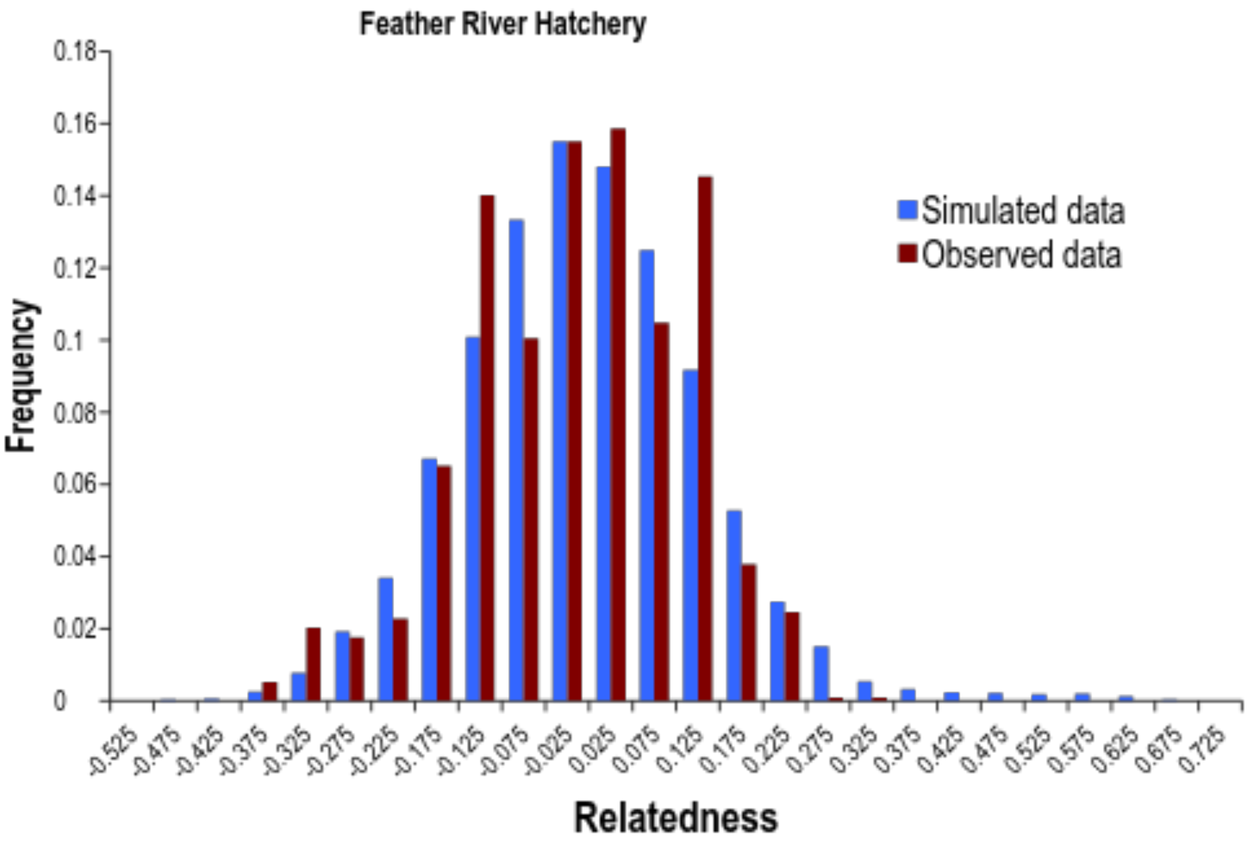
Correlation between 1st and 2nd spawn dates for iteroparous fish
R^2=0.31



Inbreeding
Central Valley steelhead

Inbreeding in hatchery mating

Clear signal of inbred matings producing fewer anadromous adult returns



Parentage-based tagging – Conclusions

-Parentage- (pedigree) based tagging is a robust and powerful alternative to other tags, and is particularly useful in iteroparous species.

-Pedigrees that come with tag recoveries are valuable

-Inference about life history of hatchery stocks has already led to management change

-Return/spawn timing highly heritable in steelhead

-About 60% of returning adult Chinook and steelhead are singletons, but only about 30% of coho salmon have no full siblings amongst returning adults

-Inbreeding causing some, but only a modest amount of, mortality, because of use of genetic broodstock management with coho programs

-Iteroparity rates are similar to those in other hatchery stocks. Mostly females .

Parentage-based tagging – The Way Forward

-Educate agency staff

-Evaluate operational constraints

-Evaluate remaining technical issues and refine protocols

-Immediately expand use in steelhead and other untagged stocks

-Reduce genotyping costs and turn-around time

-Establish shared databases.

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